WHAT IS CLAIMED IS:

1. A substantially purified single or two chain polypeptide, comprising the protease domain of a type-II membrane-type serine protease 7 (MTSP7) or a catalytically active portion thereof.

2. The polypeptide of claim 1 that is an activated two chain protein.

3. A polypeptide of claim 1 selected from the group consisting of

a polypeptide that comprises a sequence of amino acids encoded by the sequence of nucleotides set forth in SEQ ID No. 15;

polypeptide that comprises a sequence of amino acids encoded by the sequence of nucleotides set forth in SEQ ID No. 17;

a polypeptide that comprises a sequence of amino acids encoded by a sequence of nucleotides that hybridizes under conditions of high stringency to the sequence of nucleotides set forth in SEQ ID No. 15 or 17;

a polypeptide that comprises the sequence of amino acids set forth as amino acids 206-438 of SEQ ID No. 16;

a polypeptide that comprises a sequence of amino acids having at least about 90% sequence identity with the sequence of amino acids set forth in SEQ ID No. 16 or 18; and

a polypeptide that is encoded by a sequence of nucleotides that is a splice variant of the sequence set forth in SEQ ID No. 15.

4. The polypeptide of claim 1, wherein:

the MTSP7 portion of the polypeptide consists essentially of the protease domain of the MTSP7 or a catalytically active portion thereof.

5. The substantially purified polypeptide of claim 1, wherein the MTSP7 is a human polypeptide.

6. The substantially purified polypeptide of claim 1 that consists essentially of the protease domain of MTSP7 or a catalytically active portion of the protease domain of MTSP7.

7. The substantially purified polypeptide of claim 3 that consists essentially of the protease domain of MTSP7 or a catalytically active portion of the protease domain of MTSP7.

8. The substantially purified polypeptide of claim 1 that comprises the sequence of amino acids set forth in SEQ ID No. 16.

9. The substantially purified polypeptide of claim 1 that comprises the sequence of amino acids set forth in SEQ ID No. 18.

10. The substantially purified polypeptide of claim 1, wherein the protease domain comprises the sequence of amino acids set forth as amino acids 206-438 of SEQ ID No. 16.

11. The substantially purified polypeptide of claim 1 that has at least about 60%, 80%, 90% or 95% sequence identity with a polypeptide that comprises the sequence of amino acids set forth as SEQ ID No. 16 or as the sequence of amino acids set forth as SEQ ID No. 18, wherein the polypeptide is a protease.

12. A polypeptide of claim 1, wherein the protease domain portion is encoded by a nucleic acid molecule that hybridizes under conditions of high stringency along at least 70% of its full length to a nucleic acid molecule comprising a sequence of nucleotides set forth in SEQ ID No: 15 or at least one domain thereof or a catalytically active portion of the domain.

13. The polypeptide of claim 12, wherein the domain is the protease domain

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14. The polypeptide of claim 1, wherein:

the polypeptide does not comprise the complete sequence set forth in SEQ ID No. 16; and

the MTSP7 portion of the polypeptide consists essentially of the protease domain of the MTSP7 or a catalytically active portion thereof.

15. A polypeptide of claim 3 that is a mutein, wherein:

up to about 40% of the amino acids are replaced with another amino acid;

and the resulting polypeptide is a single chain or two chain polypeptide that has catalytic activity of at least 10% of the unmutated polypeptide.

16. The polypeptide of claim 15, wherein up to about 10% of the amino acids are replaced with another amino acid.

17. The polypeptide of claim 15, wherein the resulting polypeptide is a single chain or two chain polypeptide and has catalytic activity of at least 50% of the unmutated polypeptide.

18. The polypeptide of claim 15, wherein a free Cysteine in the protease domain is replaced with another amino acid.

19. The polypeptide of claim 18, wherein the replacing amino acid is a serine.

20. A nucleic acid molecule, comprising a sequence of nucleotides that encodes the polypeptide of claim 1.

21. A nucleic acid molecule, comprising a sequence of nucleotides that encodes the polypeptide of claim 3.

22. The nucleic acid molecule of claim 20 that comprises a sequence of nucleotides selected from the group consisting of:

(a) a sequence of nucleotides set forth in SEQ ID No. 15 or 17;

(b) a sequence of nucleotides that hybridizes under high stringency along its length to the sequence of nucleotides set forth in SEQ ID No. 15 or 17;

(c) degenerate codons of (a) or (b).

23. An isolated nucleic molecule that encodes a mutein of claim 15.

24. A vector comprising the nucleic acid molecule of claim 20.

25. The vector of claim 24 that is an expression vector.

26. The vector of claim 24 that is a eukaryotic vector.

27. The vector of claim 25 that includes a sequence of nucleotides that directs secretion of any polypeptide encoded by a sequence of nucleotides operatively linked thereto.

28. The vector of claim 24 that is a *Pichia* vector or an *E. coli* vector.

29. A cell, comprising the vector of claim 24.

30. The cell of claim 29 that is a prokaryotic cell.

31. The cells of claim 29 that is a eukaryotic cell.

32. The cell of claim 29 that is selected from among a bacterial cell, a yeast cell, a plant cell, an insect cell and an animal cell.

33. The cell of claim 29 that is a mammalian cell.

34. A nucleic acid molecule encoding a polypeptide of claim 6.

35. A vector, comprising nucleic acid molecule of claim 34.

36. A cell, comprising the vector of claim 35.

37. A recombinant non-human animal, wherein an endogenous gene that encodes a polypeptide of claim 1 has been deleted or inactivated by homologous recombination or insertional mutagenesis of the animal or an ancestor thereof.

38. A method for producing a polypeptide that contains a protease domain of an MTSP7 polypeptide, comprising:

culturing the cell of claim 29 under conditions whereby the encoded polypeptide is expressed by the cell; and

recovering the expressed polypeptide.

39. The method of claim 38, wherein the polypeptide is secreted into the culture medium.

40. The method of claim 38, wherein the cell is a *Pichia* cell.

41. The method of claim 38, wherein the polypeptide is expressed in the cytoplasm of the host cell.

42. A method for producing a polypeptide that contains a protease domain of a polypeptide, comprising:

culturing the cell of claim 36 under conditions whereby the encoded polypeptide is expressed by the cell; and

recovering the expressed polypeptide.

43. An antisense nucleic acid molecule that comprises at least 14 contiguous nucleotides or modified nucleotides that are complementary to a contiguous sequence of nucleotides encoding the protease domain of an MTSP7 of claim 1; or

comprises at least 16 contiguous nucleotides or modified nucleotides that are complementary to a contiguous sequence of nucleotides encoding the protease domain of an MTSP7 of claim 1; or

comprises at least 30 contiguous nucleotides or modified nucleotides that are complementary to a contiguous sequence of nucleotides encoding the protease domain of an MTSP7 of claim 1.

44. The antisense molecule of claim 43 that includes a contiguous sequence of nucleotides set forth in SEQ ID No. 15.

45. A double-stranded RNA (dsRNA) molecule that comprises at least about 21 contiguous nucleotides or modified nucleotides from the sequence of nucleotides encoding the MTSP7 of claim 1.

46. An antibody that specifically binds to the single chain form and/or two-chain form of a protease domain of the polypeptide of claim 1, or a fragment or derivative of the antibody containing a binding domain thereof, wherein the antibody is a polyclonal antibody or a monoclonal antibody.

47. The antibody of claim 46 that inhibits the enzymatic activity of the polypeptide.

48. An antibody that specifically binds to the single chain form and/or two-chain form of a protease domain of the polypeptide of claim 3, or a fragment or derivative of the antibody containing a binding domain thereof, wherein the antibody is a polyclonal antibody or a monoclonal antibody.

49. An antibody that specifically binds to the single chain form and/or two-chain form of a protease domain of the polypeptide of claim 6, or a fragment or derivative of the antibody containing a binding domain thereof, wherein the antibody is a polyclonal antibody or a monoclonal antibody.

50. A conjugate, comprising:

a) a polypeptide of claim 1, and

b) a targeting agent linked to the polypeptide directly or via a linker.

51. The conjugate of claim 50, wherein the targeting agent permits

i) affinity isolation or purification of the conjugate;

ii) attachment of the conjugate to a surface;

iii) detection of the conjugate; or

iv) targeted delivery to a selected tissue or cell.

52. A conjugate, comprising:

a) a polypeptide of claim 3; and

b) a targeting agent linked to the polypeptide directly or via a linker.

53. The conjugate of claim 52, wherein the targeting agent permits

i) affinity isolation or purification of the conjugate;

ii) attachment of the conjugate to a surface;

iii) detection of the conjugate; or

iv) targeted delivery to a selected tissue or cell.

54. A conjugate, comprising:

a) a polypeptide of claim 6; and

b) a targeting agent linked to the polypeptide directly or via a linker.

55. The conjugate of claim 54, wherein the targeting agent permits

i) affinity isolation or purification of the conjugate;

ii) attachment of the conjugate to a surface;

iii) detection of the conjugate; or

iv) targeted delivery to a selected tissue or cell.

56. A combination, comprising:

a) an agent or treatment that inhibits the catalytic activity of the polypeptide of claim 1; and

b) another treatment or agent selected from anti-tumor and anti-angiogenic treatments and agents.

57. The combination of claim 56, wherein the inhibitor and the anti-tumor and/or anti-angiogenic agent are formulated in a single pharmaceutical composition or each is formulated in separate pharmaceutical compositions.

58. The combination of claim 56, wherein the inhibitor is selected from antibodies and antisense oligonucleotides and double-stranded RNA (dsRNA).

59. A solid support comprising two or more polypeptides of claim 1 linked thereto either directly or via a linker.

60. The support of claim 59, wherein the polypeptides comprise an array.

61. The support of claim 59, wherein the polypeptides comprise a plurality of different protease domains.

62. A solid support comprising two or more nucleic acid molecules of claim 20 or oligonucleotides portions thereof linked thereto either directly or via a linker, wherein the oligonucleotides contain at least 16 nucleotides.

63. The support of claim 62, wherein the nucleic acid molecules comprise an array.

64. The support of claim 62, wherein the nucleic acid molecules comprise a plurality of molecules that encode different protease domains.

65. A method for identifying compounds that modulate the protease activity of a polypeptide, comprising:

contacting a polypeptide of claim 1 with a substrate that is proteolytically cleaved by the polypeptide, and, either simultaneously, before or after, adding a test compound or plurality thereof;

measuring the amount of substrate cleaved in the presence of the test compound; and

selecting compounds that change the amount of substrate cleaved compared to a control, whereby compounds that modulate the activity of the polypeptide are identified.

66. The method of claim 65, wherein the test compounds are small molecules, peptides, peptidomimetics, natural products, antibodies or fragments thereof that modulate the activity of the polypeptide.

67. The method of claim 65, wherein a plurality of the test substances are screened simultaneously.

68. The method of claim 65, wherein the polypeptide consists essentially of a polypeptide encoded by a sequence of nucleotides selected from the group consisting of a sequence of nucleotides that:

(a) is set forth in SEQ ID No. 17;

(b) hybridizes under conditions of high stringency to nucleic acid complementary to an mRNA transcript present in a mammalian cell that encodes MTSP7 encoded by (a);

(c) encodes a splice variant of (a) or (b); and

(d) comprises degenerate codons of the sequences of nucleotides of (a), (b) or (c).

69. The method of claim 65, wherein the polypeptide consists essentially of a polypeptide selected from the group consisting of:

a polypeptide that comprises a sequence of amino acids encoded by the sequence of nucleotides set forth in SEQ ID No. 15;

polypeptide that comprises a sequence of amino acids encoded by the sequence of nucleotides set forth in SEQ ID No. 17;

a polypeptide that comprises a sequence of amino acids encoded by a sequence of nucleotides that hybridizes under conditions of high stringency to the sequence of nucleotides set forth in SEQ ID No. 15 or 17;

a polypeptide that comprises the sequence of amino acids set forth as amino acids 206-438 of SEQ ID No. 16;

a polypeptide that comprises a sequence of amino acids having at least about 90% sequence identity with the sequence of amino acids set forth in SEQ ID No. 16 or 18; and

a polypeptide that is encoded by a sequence of nucleotides that is a splice variant of the sequence set forth in SEQ ID No. 15.

70. The method of claim 65, wherein the change in the amount of substrate cleaved is assessed by comparing the amount of substrate cleaved in the presence of the test compound with the amount of substrate cleaved in the absence of the test compound.

71. The method of claim 67, wherein a plurality of the polypeptides are linked to a solid support, either directly or via a linker.

72. The method of claim 71, wherein the polypeptides comprise an array.

73. A method of identifying a compound that specifically binds to a single-chain and/or two-chain protease domain and/or to single or two-chain full-length polypeptide, comprising:

contacting a polypeptide of claim 1 with a test compound or plurality thereof under conditions conducive to binding thereof; and

identifying compounds that specifically bind to the polypeptide single chain protease domain, or two chain form thereof, the full length or two chain form of the full length polypeptide or compounds that inhibit binding of a compound known to bind to the polypeptide single chain protease domain or two chain form thereof or the two chain form of the

full length polypeptide, wherein the known compound is contacted with the polypeptide before, simultaneously with or after the test compound.

74. The method of claim 73, wherein the polypeptide is linked either directly or indirectly via a linker to a solid support.

75. The method of claim 73, wherein the test compounds are small molecules, peptides, peptidomimetics, natural products, antibodies or fragments thereof.

76. The method of claim 73, wherein a plurality of the test substances are screened simultaneously.

77. The method of claim 73, wherein a plurality of the polypeptides are linked to a solid support.

78. The method of claim 73, wherein the polypeptide consists essentially of a polypeptide encoded by a sequence of nucleotides that:

(a) is set forth in SEQ ID No. 17;

(b) hybridizes under conditions of moderate or high stringency to nucleic acid complementary to an mRNA transcript present in a mammalian cell that encodes a MTSP7 encoded by (a);

(c) encodes a splice variant of (a) or (b); and

(d) comprises degenerate codons of the sequences of nucleotides of (a), (b) or (c).

79. A method for identifying activators of the zymogen form of an MTSP7, comprising:

contacting a zymogen form of the polypeptide of claim 1 with a substrate of the activated form of the polypeptide;

add a test compound, wherein the test compound is added before, after or simultaneously with the addition of the substrate; and

detecting cleavage of the substrate, thereby identifying compounds that activate the zymogen.

80. The method of claim 77, wherein the substrate is a chromogenic substrate.

81. The method of claim 77, wherein the substrate is a

L-pyroglutamyl-L-prolyl-L-arginine-p-nitroaniline hydrochloride.

82. The method of claim 77, wherein the test compound is a small molecule, a nucleic acid or a polypeptide.

83. A method for treating or preventing a neoplastic disease, in a mammal, comprising administering to a mammal an effective amount of an inhibitor of a polypeptide of claim 1.

84. The method of claim 83, wherein the inhibitor is an antibody that specifically binds to the polypeptide, or a fragment or derivative of the antibody containing a binding domain thereof, wherein the antibody is a polyclonal antibody or a monoclonal antibody.

85. A method for treating or preventing a neoplastic disease, in a mammal, comprising administering to a mammal an effective amount of an inhibitor of a polypeptide of claim 3.

86. A method for treating or preventing a neoplastic disease, in a mammal, comprising administering to a mammal an effective amount of an inhibitor of a polypeptide of claim 6.

87. A method of inhibiting tumor initiation, growth or progression or treating a malignant or pre-malignant condition, comprising administering an agent that inhibits activation of the zymogen form of a polypeptide of claim 1 or an activity of the activated form.

88. The method of claim 87, wherein the condition is a condition of the breast, cervix, prostate, lung, ovary or colon.

89. The method of claim 87, wherein the agent is an antisense oligonucleotide, double-stranded RNA (dsRNA) or an antibody.

90. The method of claim 87, further comprising administering another treatment or agent selected from anti-tumor and anti-angiogenic treatments or agents.

91. A method of inhibiting tumor initiation, growth or progression or treating a malignant or pre-malignant condition, comprising administering an agent that inhibits activation of the zymogen form of a polypeptide of claim 3 or an activity of the activated form.

92. The method of claim 91, wherein the condition is a condition of the breast, cervix, prostate, lung, ovary or colon.

93. The method of claim 91, wherein the agent is an antisense oligonucleotide, double-stranded RNA (dsRNA) or an antibody.

94. The method of claim 91, further comprising administering another treatment or agent selected from anti-tumor and anti-angiogenic treatments or agents.

95. A method of identifying a compound that binds to the single-chain or two-chain form of a polypeptide of claim 1, comprising:

contacting a test compound with both forms;

determining to which form the compound binds; and

if it binds to a form of polypeptide, further determining whether the compound has at least one of the following properties:

(i) inhibits activation of the single-chain zymogen form of polypeptide;

(ii) inhibits activity of the two-chain or single-chain form; and

(iii) inhibits dimerization of the polypeptide.

96. The method of claim 95, wherein both forms consist essentially of the protease domain produced by cleavage between the arginine and isoleucine in either the single- or two-chain form.

97. A method of identifying a compound that binds to the single-chain or two-chain form of a polypeptide of claim 3, comprising:

contacting a test compound with both forms;

determining to which form the compound binds; and

if it binds to a form of polypeptide, further determining whether the compound has at least one of the following properties:

(i) inhibits activation of the single-chain zymogen form of polypeptide;

(ii) inhibits activity of the two-chain or single-chain form; and

(iii) inhibits dimerization of the polypeptide.

98. The method of claim 97, wherein both forms consist essentially of the protease domain produced by cleavage between the R and I in either the single- or two-chain form.

99. A method of detecting neoplastic disease, comprising: detecting a polypeptide that comprises a polypeptide of claim 1 in a biological sample, wherein the amount detected differs from the amount of polypeptide detected from a subject who does not have neoplastic disease.

100. The method of claim 99, wherein the biological sample is selected from the group consisting of blood, urine, saliva, tears, synovial fluid, sweat, interstitial fluid, cerebrospinal fluid, ascites fluid, tumor tissue biopsy and circulating tumor cells.

101. A method of detecting neoplastic disease, comprising: detecting a polypeptide that comprises a polypeptide of claim 3 in a biological sample, wherein the amount detected differs from the amount of polypeptide detected from a subject who does not have neoplastic disease.

102. The method of claim 101, wherein the biological sample is selected from the group consisting of blood, urine, saliva, tears, synovial fluid, sweat, interstitial fluid, cerebrospinal fluid, ascites fluid, tumor tissue biopsy and circulating tumor cells.

103. A method of detecting neoplastic disease, comprising: detecting a polypeptide that comprises a polypeptide of claim 6 in a biological sample, wherein the amount detected differs from the amount of polypeptide detected from a subject who does not have neoplastic disease.

104 The method of claim 103, wherein the biological sample is selected from the group consisting of blood, urine, saliva, tears, synovial fluid, sweat, interstitial fluid, cerebrospinal fluid, ascites fluid, tumor tissue biopsy and circulating tumor cells.

105. A method of diagnosing the presence of a pre-malignant lesion, a malignancy, or other pathologic condition in a subject, comprising:

obtaining a biological sample from the subject; and

exposing it to a detectable agent that binds to a two-chain and/or single-chain form of a polypeptide of claim 1, wherein the pathological condition is characterized by the presence or absence of the two-chain or single-chain form.

106. A method of diagnosing the presence of a pre-malignant lesion, a malignancy, or other pathologic condition in a subject, comprising:

obtaining a biological sample from the subject; and

exposing it to a detectable agent that binds to a two-chain and/or single-chain form of a polypeptide of claim 3, wherein the pathological condition is characterized by the presence or absence of the two-chain or single-chain form.

107. A method of diagnosing the presence of a pre-malignant lesion, a malignancy, or other pathologic condition in a subject, comprising:

obtaining a biological sample from the subject; and

exposing it to a detectable agent that binds to a two-chain and/or single-chain form of a polypeptide of claim 6, wherein the pathological condition is characterized by the presence or absence of the two-chain or single-chain form .

108. A method of monitoring tumor progress and/or therapeutic effectiveness, comprising detecting and/or quantifying the level of a polypeptide of claim 1 in a body tissue or fluid sample.

109. The method of claim 108, wherein the tumor is tumor is a tumor of the breast, cervix, prostate, lung, ovary or colon.

110. The method of claim 108, wherein the body fluid is blood, urine, sweat, saliva, cerebrospinal fluid and synovial fluid.

111. A method of monitoring tumor progress and/or therapeutic effectiveness, comprising detecting and/or quantifying the level of a polypeptide of claim 3 in a body tissue or fluid sample.

112. The method of claim 111, wherein the tumor is tumor is a tumor of the breast, cervix, prostate, lung, ovary or colon.

113. The method of claim 111, wherein the body fluid is blood, urine, sweat, saliva, cerebrospinal fluid and synovial fluid.

114. A method of monitoring tumor progress and/or therapeutic effectiveness, comprising detecting and/or quantifying the level of a polypeptide of claim 6 in a body tissue or fluid sample.

115. The method of claim 114, wherein the tumor is tumor is a tumor of the breast, cervix, prostate, lung, ovary or colon.

116. The method of claim 114, wherein the body fluid is blood, urine, sweat, saliva, cerebrospinal fluid and synovial fluid.